

SEQUENCE LISTING

<110> ALBANG, Richard
FOLKERS, Ulrike
FRITZ, Andreas
GERHARD, Beatrix
HEINRICH, Oliver
ILGENFRITZ, Hilmar
MAIER, Dieter
SPREAFICO, Fabio
WAGNER, Christian
DE BOER, Lex
MEIMA, Roelf Bernhard

<120> NOVEL LIPASES AND USES THEREOF

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<213> *Aspergillus niger*

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Arg Thr Leu Ser Asn Trp Ser Asn Leu Thr Val Glu Thr Arg Thr Gly
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Thr Phe Ile Gly Met Leu Asn Asp Thr Tyr Pro Asp Val Arg Gln Phe
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Pro Pro His Arg Leu Asp Asn Ser Ser Arg Thr Tyr Asp Ser Thr Phe
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Asn Glu Tyr Glu Pro Glu Asn Leu Leu Leu Asn Val Gly Glu Arg Leu
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225 230 235 240

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 <213> Aspergillus niger

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<213> *Aspergillus niger*

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His Pro Ser Ala Thr Val Ile Gly Lys Ser Gly Asn Val Glu Ser Phe	
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Asn Asn Ile Pro Phe Ala Gln Ala Pro Thr Gly Ser Leu Arg Leu Lys	
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Pro Pro Gln Pro Leu Glu Thr Ala Leu Gly Thr Val Gln Ala Thr Gly	
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gcc tcg caa tcg tgt ccg cag atg tac ttc acc acg gat gag agc gaa	288
Ala Ser Gln Ser Cys Pro Gln Met Tyr Phe Thr Thr Asp Glu Ser Glu	
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Phe Pro Thr Ser Val Ile Gly Leu Leu Ala Asp Leu Pro Leu Val Gln	
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Ser Ala Thr Asn Ala Leu Glu Asp Cys Leu Asn Ile Asp Ile Arg Arg	
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Pro Ala Gly Thr Thr Ala Asp Ser Lys Leu Pro Val Leu Val Trp Ile	
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Phe Gly Gly Gly Phe Glu Leu Gly Ser Lys Ala Met Tyr Asp Gly Thr	
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Asp	Gln	Met	Ile	Leu	Tyr	Asp	Gly	Asn	Ile	Thr	Tyr	Lys	Asp	Lys	Pro	
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Leu	Phe	Arg	Gly	Ala	Ile	Met	Asp	Ser	Gly	Ser	Val	Val	Pro	Ala	Asp	
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Pro	Val	Asp	Gly	Val	Lys	Gly	Gln	Gln	Val	Tyr	Asp	Ala	Val	Val	Glu	
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Glu	Leu	Val	Ala	Leu	Tyr	Pro	Asp	Thr	Thr	Thr	Tyr	Gly	Ser	Pro	Phe	
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Arg	Thr	Gly	Ala	Ala	Asn	Asn	Trp	Tyr	Pro	Gln	Phe	Lys	Arg	Leu	Ala	
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Asp	Leu	Leu	Gln	Val	Phe	Tyr	Gly	Ile	Lys	Pro	Asn	Tyr	Ala	Ala	Ser	
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tatcgtgcag	ccgggaaaata	atctaacggt	gattgcatcg	cgggccgacg	aattggtcac	1800
cccaaccacc	acctccttcg	tgcataga	tggggtgacc	aatgaatggg	tgcaagacac	1860
ttgtcctcta	gaccctgtcg	gtcatatcgg	tgaggcatac	gatctgaacg	tctggaattt	1920
ggtcaaaaac	gccttggact	ctacgccgaa	gcgtgagttc	gtctgctcgc	tgggatctcc	1980
cggcaggtga	gactatcatc	ttctgaaaat	ttgtatataa	gcatttatat	ttggataccc	2040
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<210> 14
 <211> 834
 <212> DNA
 <213> *Aspergillus niger*

<220>
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 <222> (1)..(834)

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Met	Arg	Leu	Ser	Ser	Leu	Ala	Leu	Ala	Ser	Ser	Ala	Ile	Leu	Pro	Ala	
1			5						10					15		
tta	ggc	tac	agc	atc	aac	gac	ttc	tcc	tgc	aat	agc	acc	gaa	cac	ccg	96
Leu	Gly	Tyr	Ser	Ile	Asn	Asp	Phe	Ser	Cys	Asn	Ser	Thr	Glu	His	Pro	
			20					25					30			
aat	cca	gtt	gtg	ctc	cta	cat	ggg	cta	ggc	gcc	acc	tac	tac	gaa	gac	144
Asn	Pro	Val	Val	Leu	Leu	His	Gly	Leu	Gly	Ala	Thr	Tyr	Tyr	Glu	Asp	
			35				40					45				
ttg	aat	tac	ctg	caa	ggt	tgg	cta	cag	acc	caa	ggc	tat	tgc	act	tac	192
Leu	Asn	Tyr	Leu	Gln	Gly	Trp	Leu	Gln	Thr	Gln	Gly	Tyr	Cys	Thr	Tyr	
	50					55					60					
gcc	aaa	acc	tac	ggt	gca	tat	gaa	ggc	ttc	ccc	ttt	gtc	ggc	ggc	ctc	240
Ala	Lys	Thr	Tyr	Gly	Ala	Tyr	Glu	Gly	Phe	Pro	Phe	Val	Gly	Gly	Leu	
65					70				75						80	
aag	gcc	atc	gcc	gaa	tcg	gcc	acg	gaa	atc	gcc	gcg	tac	atc	cgc	gag	288
Lys	Ala	Ile	Ala	Glu	Ser	Ala	Thr	Glu	Ile	Ala	Ala	Tyr	Ile	Arg	Glu	
				85				90					95			
gtg	aaa	gaa	aag	acg	ggc	gcc	gac	aag	att	gac	ctt	gtc	ggt	cac	tcc	336
Val	Lys	Glu	Lys	Thr	Gly	Ala	Asp	Lys	Ile	Asp	Leu	Val	Gly	His	Ser	
			100					105					110			
gaa	ggc	gcc	ttc	cag	acc	ctc	tac	gtc	cct	aag	ttc	gag	gat	ggt	atc	384
Glu	Gly	Ala	Phe	Gln	Thr	Leu	Tyr	Val	Pro	Lys	Phe	Glu	Asp	Gly	Ile	
			115				120					125				
tcg	gag	atg	ctg	gat	aag	ctg	gtg	gcc	att	gca	cct	ccc	acc	aga	ggc	432
Ser	Glu	Met	Leu	Asp	Lys	Leu	Val	Ala	Ile	Ala	Pro	Pro	Thr	Arg	Gly	
			130			135					140					
acc	aac	ttg	gcg	ggg	atc	tat	gac	atc	gca	tat	ggt	ctg	gga	aat	cta	480
Thr	Asn	Leu	Ala	Gly	Ile	Tyr	Asp	Ile	Ala	Tyr	Val	Leu	Gly	Asn	Leu	
					150					155					160	
tcg	cgc	gat	ctg	ata	ggc	gac	gtc	ctg	gat	acc	gtg	ggc	tgc	gcc	gcc	528
Ser	Arg	Asp	Leu	Ile	Gly	Asp	Val	Leu	Asp	Thr	Val	Gly	Cys	Ala	Ala	
				165				170					175			
tgt	gat	gat	ctg	ggt	ccg	gat	gga	gca	gcg	att	gac	cgc	ttg	aac	gat	576
Cys	Asp	Asp	Leu	Gly	Pro	Asp	Gly	Ala	Ala	Ile	Asp	Arg	Leu	Asn	Asp	
			180				185						190			

ggc gag cct atc gtg cag ccg gga aat aat cta acg gtg att gca tcg	624
Gly Glu Pro Ile Val Gln Pro Gly Asn Asn Leu Thr Val Ile Ala Ser	
195 200 205	
cgg tcc gac gaa ttg gtc acc cca acc acc acc tcc ttc gtg cat gaa	672
Arg Ser Asp Glu Leu Val Thr Pro Thr Thr Thr Ser Phe Val His Glu	
210 215 220	
gat ggg gtg acc aat gaa tgg gtg caa gac act tgt cct cta gac cct	720
Asp Gly Val Thr Asn Glu Trp Val Gln Asp Thr Cys Pro Leu Asp Pro	
225 230 235 240	
gtc ggt cat atc ggt gag gca tac gat ctg aac gtc tgg aat ttg gtc	768
Val Gly His Ile Gly Glu Ala Tyr Asp Leu Asn Val Trp Asn Leu Val	
245 250 255	
aaa aac gcc ttg gac tct acg ccg aag cgt gag ttc gtc tgc tcg ctg	816
Lys Asn Ala Leu Asp Ser Thr Pro Lys Arg Glu Phe Val Cys Ser Leu	
260 265 270	
gga tct ccc ggc agg tga	834
Gly Ser Pro Gly Arg	
275	

<210> 15
 <211> 277
 <212> PRT
 <213> Aspergillus niger

<400> 15

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Leu Gly Tyr Ser Ile Asn Asp Phe Ser Cys Asn Ser Thr Glu His Pro	
20 25 30	
Asn Pro Val Val Leu Leu His Gly Leu Gly Ala Thr Tyr Tyr Glu Asp	
35 40 45	
Leu Asn Tyr Leu Gln Gly Trp Leu Gln Thr Gln Gly Tyr Cys Thr Tyr	
50 55 60	
Ala Lys Thr Tyr Gly Ala Tyr Glu Gly Phe Pro Phe Val Gly Gly Leu	
65 70 75 80	
Lys Ala Ile Ala Glu Ser Ala Thr Glu Ile Ala Ala Tyr Ile Arg Glu	
85 90 95	
Val Lys Glu Lys Thr Gly Ala Asp Lys Ile Asp Leu Val Gly His Ser	
100 105 110	
Glu Gly Ala Phe Gln Thr Leu Tyr Val Pro Lys Phe Glu Asp Gly Ile	
115 120 125	
Ser Glu Met Leu Asp Lys Leu Val Ala Ile Ala Pro Pro Thr Arg Gly	
130 135 140	
Thr Asn Leu Ala Gly Ile Tyr Asp Ile Ala Tyr Val Leu Gly Asn Leu	
145 150 155 160	
Ser Arg Asp Leu Ile Gly Asp Val Leu Asp Thr Val Gly Cys Ala Ala	
165 170 175	
Cys Asp Asp Leu Gly Pro Asp Gly Ala Ala Ile Asp Arg Leu Asn Asp	
180 185 190	
Gly Glu Pro Ile Val Gln Pro Gly Asn Asn Leu Thr Val Ile Ala Ser	
195 200 205	
Arg Ser Asp Glu Leu Val Thr Pro Thr Thr Thr Ser Phe Val His Glu	
210 215 220	
Asp Gly Val Thr Asn Glu Trp Val Gln Asp Thr Cys Pro Leu Asp Pro	
225 230 235 240	
Val Gly His Ile Gly Glu Ala Tyr Asp Leu Asn Val Trp Asn Leu Val	
245 250 255	
Lys Asn Ala Leu Asp Ser Thr Pro Lys Arg Glu Phe Val Cys Ser Leu	
260 265 270	
Gly Ser Pro Gly Arg	

<210> 16
 <211> 1881
 <212> DNA
 <213> *Aspergillus niger*

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 gcacgcgaga cccgccccgg atgcttagct gaagccggca tagtccatcc ccgctcgggc 120
 gtgatgccca acggtcactg gaggagaggt gcagggagga tgccgttgca tgaatcaagc 180
 ccggggtttg actttcatcc gctcgtttcc tactggcggg ttccgccctct ccatcgaagc 240
 cacggatcct tccatccgga tcttggcaga acagtgagga agcagagctt gggtatagta 300
 gaaattatta ataccgagct ggtctgcca tttttcccaa accttccctc tttccatccc 360
 tctcgccctg caccctctt atcctccctc ccgccatgta tatccctcg gtgctgcttc 420
 tggcgcgcgag cctgttccat ggcgcaacgg cgctgcccac gcccggtcc acgcccaccc 480
 cgcccagcca ggatccctgg tacagtgcgc ccgagggctt cgaggaggct gatcccggtg 540
 ccactctgcg cgtgcggccc gcgcccggca acttgaccgt ggtagtgaggc aatgcgtcgg 600
 cggcctacaa catcctctac cgcactacag acagtcagta caagccctcc tgggctgtga 660
 ccacctgct ggtgcccccc gtggcgcct ccgcgcgct caaccagagt gtctgtctct 720
 cccaccagat gcctacgat tcgttcgacg tcaatgccag tcccagctac gccatgtaca 780
 ccagcccgcc ctccgatatt atcctcgccc tgcagcgcgg ctggttcggt aacgtccccg 840
 attacgaggg ccccaatgcc tctttaccg ccggtgtgca gtccggccat gccaccctcg 900
 actcgggtcc cagcgtgctc gcctccggat tcggcctgaa cgaggacgcc cagtacgctc 960
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 acgctcccga gttgaacatt gccggtctgg ccgtgggtgg tctcactccc aatgttacca 1080

 gcgtcatgga cacggtgacc tcgaccatca gtgcgggact catccccgcc gccgccctgg 1140
 gtctgtcgag ccagcaccac gagacctacg agttcatcct cagccagctc aagacgacgg 1200
 gacctacaa ccgcacagga ttcttagccg ccaaggacct gacctgtcc gaggcggagg 1260
 tcttctacgc cttccagaac atcttcgatt actttgtcaa cggatcggcc acgttccagg 1320
 cggaggtggt gcagaaggcg ctgaaccagg acggatacat gggctaccat gggttccgcg 1380
 agatgccggg gctcgcgtac aaggctattc acgatgagat cagtcccatc caggatacgg 1440
 atcgcgtgat caagcgctac tgttgtctgg gattgaacat cttgtatgag cggaacacca 1500
 tcggtggcca ctcggcagag caggtgaatg gcaacgccag ggcgtggaac tggttgacga 1560
 gcattttcga cggaacgtat gcgcagcagt acaagaccga ggggtgcacg atccgcaatg 1620
 tcactctgaa cagcacttcc tccgtttatt agagaggggg ctggtgttat gtgaataatg 1680
 ctgaagatgg ctgtgtatgg acggtccgct ctcctgtata gtaatgggct aatgcatgcg 1740
 gcttcatgaa catggtacga aagattagat tatgtatata gtgtggaagt ggtaatgatg 1800
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 aatgactact ggcacatctg c 1881

<210> 17
 <211> 1257
 <212> DNA
 <213> *Aspergillus niger*

<220>
 <221> CDS
 <222> (1)..(1257)

<400> 17
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 gca acg gcg ctg ccc acg ccc ggc tcc acg ccc atc ccg ccc agc cag 96
 Ala Thr Ala Leu Pro Thr Pro Gly Ser Thr Pro Ile Pro Pro Ser Gln
 20 25 30
 gat ccc tgg tac agt gcg ccc gag ggc ttc gag gag gct gat ccc ggt 144

Asp	Pro	Trp	Tyr	Ser	Ala	Pro	Glu	Gly	Phe	Glu	Glu	Ala	Asp	Pro	Gly	
		35					40					45				
gcc	atc	ctg	cgc	gtg	cgg	ccc	gcg	ccc	ggc	aac	ttg	acc	gtg	gta	gtg	192
Ala	Ile	Leu	Arg	Val	Arg	Pro	Ala	Pro	Gly	Asn	Leu	Thr	Val	Val	Val	
		50					55				60					
ggc	aat	gcg	tcg	gcg	gcc	tac	aac	atc	ctc	tac	cgc	act	aca	gac	agt	240
Gly	Asn	Ala	Ser	Ala	Ala	Tyr	Asn	Ile	Leu	Tyr	Arg	Thr	Thr	Asp	Ser	
		65				70				75					80	
cag	tac	aag	ccc	tcc	tgg	gct	gtg	acc	acc	ctg	ctg	gtg	ccc	ccc	gtg	288
Gln	Tyr	Lys	Pro	Ser	Trp	Ala	Val	Thr	Leu	Leu	Val	Pro	Pro	Val	Val	
				85					90					95		
gcc	gcc	tcc	gcc	gcc	gtc	aac	cag	agt	gtc	ctg	ctc	tcc	cac	cag	atc	336
Ala	Ala	Ser	Ala	Ala	Val	Asn	Gln	Ser	Val	Leu	Leu	Ser	His	Gln	Ile	
			100					105					110			
gcc	tac	gat	tcg	ttc	gac	gtc	aat	gcc	agt	ccc	agc	tac	gcc	atg	tac	384
Ala	Tyr	Asp	Ser	Phe	Asp	Val	Asn	Ala	Ser	Pro	Ser	Tyr	Ala	Met	Tyr	
		115				120						125				
acc	agc	ccg	ccc	tcc	gat	att	atc	ctc	gcc	ctg	cag	cgc	ggc	tgg	ttc	432
Thr	Ser	Pro	Pro	Ser	Asp	Ile	Ile	Leu	Ala	Leu	Gln	Arg	Gly	Trp	Phe	
		130				135					140					
gtt	aac	gtc	ccc	gat	tac	gag	ggc	ccc	aat	gcc	tct	ttc	acc	gcc	ggc	480
Val	Asn	Val	Pro	Asp	Tyr	Glu	Gly	Pro	Asn	Ala	Ser	Phe	Thr	Ala	Gly	
		145			150					155					160	
gtg	cag	tcc	ggc	cat	gcc	acc	ctc	gac	tcg	gtc	cgc	agc	gtg	ctc	gcc	528
Val	Gln	Ser	Gly	His	Ala	Thr	Leu	Asp	Ser	Val	Arg	Ser	Val	Leu	Ala	
				165				170						175		
tcc	gga	ttc	ggc	ctg	aac	gag	gac	gcc	cag	tac	gct	ctg	tgg	ggc	tac	576
Ser	Gly	Phe	Gly	Leu	Asn	Glu	Asp	Ala	Gln	Tyr	Ala	Leu	Trp	Gly	Tyr	
			180					185					190			
tct	ggc	ggc	gcc	ttg	gcc	agc	gaa	tgg	gct	gct	gaa	ctg	cag	atg	caa	624
Ser	Gly	Gly	Ala	Leu	Ala	Ser	Glu	Trp	Ala	Ala	Glu	Leu	Gln	Met	Gln	
		195					200					205				
tac	gct	ccc	gag	ttg	aac	att	gcc	ggc	ctg	gcc	gtg	ggc	ggc	ctc	act	672
Tyr	Ala	Pro	Glu	Leu	Asn	Ile	Ala	Gly	Leu	Ala	Val	Gly	Gly	Leu	Thr	
		210			215						220					
ccc	aat	gtt	acc	agc	gtc	atg	gac	acg	gtg	acc	tcg	acc	atc	agt	gcg	720
Pro	Asn	Val	Thr	Ser	Val	Met	Asp	Thr	Val	Thr	Ser	Thr	Ile	Ser	Ala	
		225			230					235				240		
gga	ctc	atc	ccc	gcc	gcc	gcc	ctg	ggc	ctg	tcg	agc	cag	cac	ccc	gag	768
Gly	Leu	Ile	Pro	Ala	Ala	Ala	Leu	Gly	Leu	Ser	Ser	Gln	His	Pro	Glu	
			245					250						255		
acc	tac	gag	ttc	atc	ctc	agc	cag	ctc	aag	acg	acg	gga	ccc	tac	aac	816
Thr	Tyr	Glu	Phe	Ile	Leu	Ser	Gln	Leu	Lys	Thr	Thr	Gly	Pro	Tyr	Asn	
			260				265						270			
cgc	aca	gga	ttc	cta	gcc	gcc	aag	gac	ctg	acc	ctg	tcc	gag	gcg	gag	864
Arg	Thr	Gly	Phe	Leu	Ala	Ala	Lys	Asp	Leu	Thr	Leu	Ser	Glu	Ala	Glu	
		275					280						285			
gtc	ttc	tac	gcc	ttc	cag	aac	atc	ttc	gat	tac	ttt	gtc	aac	gga	tcg	912
Val	Phe	Tyr	Ala	Phe	Gln	Asn	Ile	Phe	Asp	Tyr	Phe	Val	Asn	Gly	Ser	
		290				295					300					
gcc	acg	ttc	cag	gcg	gag	gtg	gtg	cag	aag	gcg	ctg	aac	cag	gac	gga	960
Ala	Thr	Phe	Gln	Ala	Glu	Val	Val	Gln	Lys	Ala	Leu	Asn	Gln	Asp	Gly	
		305			310					315					320	
tac	atg	ggc	tac	cat	ggg	ttc	ccg	cag	atg	ccg	gtg	ctc	gcg	tac	aag	1008
Tyr	Met	Gly	Tyr	His	Gly	Phe	Pro	Gln	Met	Pro	Val	Leu	Ala	Tyr	Lys	
				325					330					335		
gct	att	cac	gat	gag	atc	agt	ccc	atc	cag	gat	acg	gat	cgc	gtg	atc	1056
Ala	Ile	His	Asp	Glu	Ile	Ser	Pro	Ile	Gln	Asp	Thr	Asp	Arg	Val	Ile	
			340					345					350			
aag	cgc	tac	tgt	ggc	ctg	gga	ttg	aac	atc	ttg	tat	gag	cgc	aac	acc	1104
Lys	Arg	Tyr	Cys	Gly	Leu	Gly	Leu	Asn	Ile	Leu	Tyr	Glu	Arg	Asn	Thr	

355	360	365	
atc ggt ggc cac tcg gca gag cag gtg aat ggc aac gcc agg gcg tgg			1152
Ile Gly His Ser Ala Glu Gln Val Asn Gly Asn Ala Arg Ala Trp			
370	375	380	
aac tgg ttg acg agc att ttc gac gga acg tat gcg cag cag tac aag			1200
Asn Trp Leu Thr Ser Ile Phe Asp Gly Thr Tyr Ala Gln Gln Tyr Lys			
385	390	395	400
acc gag ggg tgc acg atc cgc aat gtc act ctg aac acg act tcc tcc			1248
Thr Glu Gly Cys Thr Ile Arg Asn Val Thr Leu Asn Thr Thr Ser Ser			
	405	410	415
gtt tat tag			1257
Val Tyr			

<210> 18
 <211> 418
 <212> PRT
 <213> *Aspergillus niger*

<400> 18

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Asp Pro Trp Tyr Ser Ala Pro Glu Gly Phe Glu Glu Ala Asp Pro Gly	
35 40 45	
Ala Ile Leu Arg Val Arg Pro Ala Pro Gly Asn Leu Thr Val Val Val	
50 55 60	
Gly Asn Ala Ser Ala Ala Tyr Asn Ile Leu Tyr Arg Thr Thr Asp Ser	
65 70 75 80	
Gln Tyr Lys Pro Ser Trp Ala Val Thr Thr Leu Leu Val Pro Pro Val	
85 90 95	
Ala Ala Ser Ala Ala Val Asn Gln Ser Val Leu Leu Ser His Gln Ile	
100 105 110	
Ala Tyr Asp Ser Phe Asp Val Asn Ala Ser Pro Ser Tyr Ala Met Tyr	
115 120 125	
Thr Ser Pro Pro Ser Asp Ile Ile Leu Ala Leu Gln Arg Gly Trp Phe	
130 135 140	
Val Asn Val Pro Asp Tyr Glu Gly Pro Asn Ala Ser Phe Thr Ala Gly	
145 150 155 160	
Val Gln Ser Gly His Ala Thr Leu Asp Ser Val Arg Ser Val Leu Ala	
165 170 175	
Ser Gly Phe Gly Leu Asn Glu Asp Ala Gln Tyr Ala Leu Trp Gly Tyr	
180 185 190	
Ser Gly Gly Ala Leu Ala Ser Glu Trp Ala Ala Glu Leu Gln Met Gln	
195 200 205	
Tyr Ala Pro Glu Leu Asn Ile Ala Gly Leu Ala Val Gly Gly Leu Thr	
210 215 220	
Pro Asn Val Thr Ser Val Met Asp Thr Val Thr Ser Thr Ile Ser Ala	
225 230 235 240	
Gly Leu Ile Pro Ala Ala Ala Leu Gly Leu Ser Ser Gln His Pro Glu	
245 250 255	
Thr Tyr Glu Phe Ile Leu Ser Gln Leu Lys Thr Thr Gly Pro Tyr Asn	
260 265 270	
Arg Thr Gly Phe Leu Ala Ala Lys Asp Leu Thr Leu Ser Glu Ala Glu	
275 280 285	
Val Phe Tyr Ala Phe Gln Asn Ile Phe Asp Tyr Phe Val Asn Gly Ser	
290 295 300	
Ala Thr Phe Gln Ala Glu Val Val Gln Lys Ala Leu Asn Gln Asp Gly	
305 310 315 320	
Tyr Met Gly Tyr His Gly Phe Pro Gln Met Pro Val Leu Ala Tyr Lys	

attgtggcca	gtgagcgatt	ttacaagccg	gtcaagtacc	cgactaagaa	cattaagacg	2520
cccattgtcc	tggtgtatgg	cggtagcgat	agtcctcggtg	atatcaacgt	gatgttgtcc	2580
gagctccctc	gcgggaccgt	ggcgaaggaa	atcccgcagt	atgagcattt	agatttcttg	2640
tgggcgcggtg	atgtggacca	attggtattc	aaccatgtct	tcgaagcgct	ggagcggtac	2700
agctcggaga	atcagaaagg	gacattgatg	gagaaggtta	atggtgccgc	gggcacatat	2760
gtaccgacat	aaagtacgag	gtcctgcacc	aatgaagaca	cgcataatc		2809

<210> 20

<211> 1413

<212> DNA

<213> *Aspergillus niger*

<220>

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<400> 20

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1			5						10				15					
gcc	ctt	ttt	ggg	tcg	ctg	att	ttg	gta	ttg	ctg	gaa	tgg	g	tt	ata	cat	96	
Ala	Leu	Phe	Gly	Ser	Leu	Ile	Leu	Val	Leu	Leu	Glu	Trp	Val	Ile	His			
			20					25					30					
att	atc	aca	ttc	tgt	ctg	cct	gaa	cct	gtt	att	aag	ttc	tgt	tac	gat		144	
Ile	Ile	Thr	Phe	Cys	Leu	Pro	Glu	Pro	Val	Ile	Lys	Phe	Cys	Tyr	Asp			
			35				40					45						
cga	tcc	aag	act	atc	ttc	aac	gcc	ttc	att	cct	ccc	gat	gac	ccg	gct		192	
Arg	Ser	Lys	Thr	Ile	Phe	Asn	Ala	Phe	Ile	Pro	Pro	Asp	Asp	Pro	Ala			
			50			55					60							
aag	cg	g	ggt	aaa	gaa	gag	aaa	att	gct	gcg	tcg	gtt	gct	ctg	gcg	tcg	240	
Lys	Arg	Gly	Lys	Glu	Glu	Lys	Ile	Ala	Ala	Ser	Val	Ala	Leu	Ala	Ser			
65				70			75						80					
gac	ttc	acg	gat	ata	tgc	gcg	ctg	ttc	gga	tat	gag	gcg	gag	gaa	cat		288	
Asp	Phe	Thr	Asp	Ile	Cys	Ala	Leu	Phe	Gly	Tyr	Glu	Ala	Glu	Glu	His			
				85				90					95					
atc	gtc	cag	aca	ggg	gat	ggc	tat	ctg	ctt	ggt	ctg	cac	cga	ctg	ccc		336	
Ile	Val	Gln	Thr	Gly	Asp	Gly	Tyr	Leu	Leu	Gly	Leu	His	Arg	Leu	Pro			
			100				105						110					
tat	cg	aaa	gga	gag	gag	ggg	agg	aag	atc	aac	cag	ggc	gaa	ggg	agc		384	
Tyr	Arg	Lys	Gly	Glu	Glu	Gly	Arg	Lys	Ile	Asn	Gln	Gly	Glu	Gly	Ser			
			115				120					125						
atc	aag	aag	aag	gtc	gtc	tat	ctc	cac	cat	ggt	ctc	atg	atg	tgc	agt		432	
Ile	Lys	Lys	Lys	Val	Val	Tyr	Leu	His	His	Gly	Leu	Met	Met	Cys	Ser			
				130			135					140						
gaa	gtc	tgg	atc	tgt	ctg	tca	gag	gag	cag	cga	tgc	ctt	ccg	ttt	caa		480	
Glu	Val	Trp	Ile	Cys	Leu	Ser	Glu	Glu	Gln	Arg	Cys	Leu	Pro	Phe	Gln			
				145		150				155				160				
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Leu	Val	Glu	Arg	Gly	Tyr	Asp	Val	Trp	Leu	Gly	Asn	Asn	Arg	Gly	Asn			
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Lys	Tyr	Ser	Lys	Lys	Ser	Val	Lys	His	Ser	Pro	Leu	Ser	Asn	Glu	Phe			
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tgg	gac	ttt	tcg	atc	gat	cag	ttc	tcg	ttc	cat	gat	atc	cca	gac	agc		624	
Trp	Asp	Phe	Ser	Ile	Asp	Gln	Phe	Ser	Phe	His	Asp	Ile	Pro	Asp	Ser			
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Gly Phe Ser Gln Gly Thr Ala Gln Ala Phe Ala Thr Leu Ser Ile His			
225	230	235	240
cct ttg ttg aat cag aag atc gat gtc ttt gtg gct ctc gcg ccg gca			768
Pro Leu Leu Asn Gln Lys Ile Asp Val Phe Val Ala Leu Ala Pro Ala			
245	250	255	
atg gct ccg aca ggt ctt cca aat cat ctc gtg gac tcg ctc atg aag			816
Met Ala Pro Thr Gly Leu Pro Asn His Leu Val Asp Ser Leu Met Lys			
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gct tcg ccg aac ttc ctg ttt ctg ctg ttt ggc aga cgc agc atc ctt			864
Ala Ser Pro Asn Phe Leu Phe Leu Phe Gly Arg Arg Ser Ile Leu			
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Ser Ser Thr Thr Met Trp Gln Thr Ile Leu Tyr Pro Pro Ile Phe Val			
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Trp Ile Ile Asp Thr Ser Leu Arg Gly Leu Phe Asn Trp Arg Cys Lys			
305	310	315	320
aac atc agc cgc tgg cag aag ctg gca ggg tac ctg cat ctg ttt tcc			1008
Asn Ile Ser Arg Trp Gln Lys Leu Ala Gly Tyr Leu His Leu Phe Ser			
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Phe Thr Ser Thr Lys Ser Val Val His Trp Phe Gln Ile Ile Arg His			
340	345	350	
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Arg Asn Phe Gln Phe Tyr Asp Asp Glu Ile His Ala Pro Leu Ser Ile			
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Val Ala Ser Glu Arg Phe Tyr Lys Pro Val Lys Tyr Pro Thr Lys Asn			
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Ile Lys Thr Pro Ile Val Leu Leu Tyr Gly Gly Ser Asp Ser Leu Val			
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gat atc aac gtg atg ttg tcc gag ctc cct cgc ggg acc gtg gcg aag			1248
Asp Ile Asn Val Met Leu Ser Glu Leu Pro Arg Gly Thr Val Ala Lys			
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Glu Ile Pro Gln Tyr Glu His Leu Asp Phe Leu Trp Ala Arg Asp Val			
420	425	430	
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Asp Gln Leu Val Phe Asn His Val Phe Glu Ala Leu Glu Arg Tyr Ser			
435	440	445	
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Ser Glu Asn Gln Lys Gly Thr Leu Met Glu Lys Val Asn Gly Ala Ala			
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 <213> Aspergillus niger

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Ile	Ile	Thr	Phe	Cys	Leu	Pro	Glu	Pro	Val	Ile	Lys	Phe	Cys	Tyr	Asp		
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Lys	Arg	Gly	Lys	Glu	Glu	Lys	Ile	Ala	Ala	Ser	Val	Ala	Leu	Ala	Ser		
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Asp	Phe	Thr	Asp	Ile	Cys	Ala	Leu	Phe	Gly	Tyr	Glu	Ala	Glu	Glu	His		
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Lys	Tyr	Ser	Lys	Lys	Ser	Val	Lys	His	Ser	Pro	Leu	Ser	Asn	Glu	Phe		
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Ala	Ser	Pro	Asn	Phe	Leu	Phe	Leu	Leu	Phe	Gly	Arg	Arg	Ser	Ile	Leu		
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Ser	Ser	Thr	Thr	Met	Trp	Gln	Thr	Ile	Leu	Tyr	Pro	Pro	Ile	Phe	Val		
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Trp	Ile	Ile	Asp	Thr	Ser	Leu	Arg	Gly	Leu	Phe	Asn	Trp	Arg	Cys	Lys		
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<213> *Aspergillus niger*

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Leu Leu Phe Ala Gln Gln Leu Ala Ser His Pro Thr Glu Gln Ile Gln
20      25      30
gcc att ctg gct ccg tgg gtc ccg gcc gca cta caa gat gtc gtg ctc      144
Ala Ile Leu Ala Pro Trp Val Pro Ala Ala Leu Gln Asp Val Val Leu
35      40      45
tat aat cga cct cgc gtc ata atc ccc cag ggc act gtc ggc acg      192
Tyr Asn Arg Pro Arg Val Ile Ile Pro Gln Gly Thr Val Val Gly Thr
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Thr Leu Thr Asp Thr Leu Lys Ser Pro Val Asp Ala Phe Arg Gly Ile
65      70      75      80
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Pro Tyr Ala Leu Pro Pro Ile Gly Asp Arg Arg Phe Arg Arg Ala Glu
85      90      95
gct gtc cat gcg acg gac gag att atc gat gct agt gaa ttc ggc cca      336
Ala Val His Ala Thr Asp Glu Ile Ile Asp Ala Ser Glu Phe Gly Pro
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agg tgc cct gga aag cag ctc ttg aat cca aat gac ata ggt ggt gat      384
Arg Cys Pro Gly Lys Gln Leu Leu Asn Pro Asn Asp Ile Gly Gly Asp
115      120      125
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130      135      140
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180      185      190
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195      200      205
aac cta ggc ctc cat gac cag atc ctc ctg ctg caa tgg gtc caa gaa      672
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210      215      220
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225      230      235      240
ctc tcc gcc ggc gcg cac tcc ata gcc cac cac atc atg aac tac aac      768
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245      250      255
cca cca aac acc ccc ctc ttt cac cgc gcc atc atc gaa tcc ggc gcc      816
Pro Pro Asn Thr Pro Leu Phe His Arg Ala Ile Ile Glu Ser Gly Ala
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Gln Phe Thr Asp Phe Leu Thr Glu Thr Gly Cys Thr Asn Leu Pro Asp	
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Thr Ala Ile Leu Pro Cys Leu Arg Ala Leu Pro Ser Ser Ala Ile Thr	
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acc gcc tcc atc tcc gtc ttc gac aaa tac aac ccc tcc atc cgc tgg	1008
Thr Ala Ser Ile Ser Val Phe Asp Lys Tyr Asn Pro Ser Ile Arg Trp	
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Tyr Ala Thr Ala Ser Pro Tyr Leu Glu Thr Arg Pro Ile Pro Ser Leu	
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Cys Gly Glu Pro Val Phe Leu Tyr Arg Trp Ala Leu Asn Lys Thr Val	
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Phe His Ala Tyr Val Thr Ser Phe Val Val His Gly Asp Pro Asn Val	
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 <213> Aspergillus niger

<400> 24

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Thr	Leu	Thr	Asp	Thr	Leu	Lys	Ser	Pro	Val	Asp	Ala	Phe	Arg	Gly	Ile
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Phe Leu Tyr Ser Gln Glu Val Ala Asp Glu Gly Ser Ala Asn Leu Gly	
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Val Ser Ser Gln Asn Pro Thr Val Asp Leu Gly Tyr Thr Arg Tyr Lys
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Gly Lys Ser Leu Pro Asn Gly Ile Ser Gln Trp Leu Gly Ile Arg Tyr
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Ala Ala Ala Pro Thr Gly Ser Leu Arg Phe Ser Ala Pro Gln Asp Pro
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Asp Thr Val Asp Gly Val Gln Glu Ala Phe Lys His Gly Pro Arg Cys
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Ser Pro Asn Tyr Asn Gly Thr Gly Leu Ile Glu Ala Ala Asn Met Ser	
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 Ser Glu Asp Cys Leu Tyr Leu Asn Val Val Arg Pro Ala Glu Tyr Asp
 100 105 110
 aat gcc agt ctt cca gtc ctt gta tgg att cat ggc ggt ggc ttc gca 384
 Asn Ala Ser Leu Pro Val Leu Val Trp Ile His Gly Gly Gly Phe Ala
 115 120 125
 caa ggc ggc act ccc gac ctt cga tac aat ctt aca ttt att gtt gaa 432
 Gln Gly Gly Thr Pro Asp Leu Arg Tyr Asn Leu Thr Phe Ile Val Glu
 130 135 140
 cac tcg gtc aat atc ggc cag cca att atc gca gtg agc gtt gcc tat 480
 His Ser Val Asn Ile Gly Gln Pro Ile Ile Ala Val Ser Val Ala Tyr
 145 150 155 160
 cgt ctc ggt cct tgg ggt ttc ttc aat ggg gtc gag ctc gcc aat gag 528
 Arg Leu Gly Pro Trp Gly Phe Phe Asn Gly Val Glu Leu Ala Asn Glu
 165 170 175
 gga tcg tta aat ctc ggg ctg aag gac cag cgc ttg gcc ctg cat tgg 576
 Gly Ser Leu Asn Leu Gly Leu Lys Asp Gln Arg Leu Ala Leu His Trp
 180 185 190
 gtg aaa gag aac att gca ggt ttc ggt ggc gac cct agt aaa gtc gtg 624
 Val Lys Glu Asn Ile Ala Gly Phe Gly Gly Asp Pro Ser Lys Val Val
 195 200 205
 att tac gga caa agt gcc ggc tcc gaa agc gtg gga tac caa atc cgc 672
 Ile Tyr Gly Gln Ser Ala Gly Ser Glu Ser Val Gly Tyr Gln Ile Arg
 210 215 220
 gcg tac aac ggc cga gat gac ggg ctc ttc cgc gga ggc atg atg gag 720
 Ala Tyr Asn Gly Arg Asp Asp Gly Leu Phe Arg Gly Gly Met Met Glu
 225 230 235 240
 tcc ggc gcg gtg tta cct ggc agt gcc ttg aac ctc acc tgg aca tat 768
 Ser Gly Ala Val Leu Pro Gly Ser Ala Leu Asn Leu Thr Trp Thr Tyr
 245 250 255

gag cct tgg ttc cag caa ata gca gac gag gca gga tgt tcc cag acc	816
Glu Pro Trp Phe Gln Gln Ile Ala Asp Glu Ala Gly Cys Ser Gln Thr	
260 265 270	
acc cgc aaa ctg gac tgt cta cgc cgc acg ccc ttc aca gtc cta aac	864
Thr Arg Lys Leu Asp Cys Leu Arg Arg Thr Pro Phe Thr Val Leu Asn	
275 280 285	
aac att ctg aac acc acc gcc aac gac acg acg cct tac aac tgg agg	912
Asn Ile Leu Asn Thr Thr Ala Asn Asp Thr Thr Pro Tyr Asn Trp Arg	
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ccc aca gtg gac ggt gac ttc gta gcg cga tat ccc agc gag caa ctc	960
Pro Thr Val Asp Gly Asp Phe Val Ala Arg Tyr Pro Ser Glu Gln Leu	
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Asp Thr Gly Asp Phe Val Lys Val Pro Ile Ile Ile Gly Tyr Thr Thr	
325 330 335	
gac gaa gga aca aca gag tgc cca gaa cca gtg aac acc acc gcc gaa	1056
Asp Glu Gly Thr Thr Glu Cys Pro Glu Pro Val Asn Thr Thr Ala Glu	
340 345 350	
tta aaa gaa tac ctc agc tca aca aca acc tac ggc tgg gcc ctc gac	1104
Leu Lys Glu Tyr Leu Ser Ser Thr Thr Thr Tyr Gly Trp Ala Leu Asp	
355 360 365	
tca cag gta gta tcc tcg ctc ctg gac ctc tac ccc aac acc acc tcc	1152
Ser Gln Val Val Ser Ser Leu Leu Asp Leu Tyr Pro Asn Thr Thr Ser	
370 375 380	
ttc ggc atc cca tca tcc gaa gaa ctc ggc ggc aac gtc acc ttc cca	1200
Phe Gly Ile Pro Ser Ser Glu Glu Leu Gly Gly Asn Val Thr Phe Pro	
385 390 395 400	
cag ccc tac ggc gcc gca ttc cgc cag acg gca gca tac tac ggc gac	1248
Gln Pro Tyr Gly Ala Ala Phe Arg Gln Thr Ala Ala Tyr Tyr Gly Asp	
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gcc cag ttc ata gcc gcg acg cgc tac acc tgt gag cta tgg gcg gca	1296
Ala Gln Phe Ile Ala Ala Thr Arg Tyr Thr Cys Glu Leu Trp Ala Ala	
420 425 430	
cat aac ctg aca gca tat tgc tac cga ttc aac acc aag aca gac gat	1344
His Asn Leu Thr Ala Tyr Cys Tyr Arg Phe Asn Thr Lys Thr Asp Asp	
435 440 445	
tac aac agg gaa gaa ggc gtg gcg cat ttc tcg gac gtg atc ttc atc	1392
Tyr Asn Arg Glu Glu Gly Val Ala His Phe Ser Asp Val Ile Phe Ile	
450 455 460	
ttc aac aac ctt aat ggt tat ggg ttc agt ccg aac ccg ttc acc aat	1440
Phe Asn Asn Leu Asn Gly Tyr Gly Phe Ser Pro Asn Pro Phe Thr Asn	
465 470 475 480	
gct cca gag agc tat act gag ctt agc tac ctc atg tcc ggc tcg tgg	1488
Ala Pro Glu Ser Tyr Thr Glu Leu Ser Tyr Leu Met Ser Gly Ser Trp	
485 490 495	
atc agc ttc act aat agt ctg gat cct aat aag tgg act ggt cgc gga	1536
Ile Ser Phe Thr Asn Ser Leu Asp Pro Asn Lys Trp Thr Gly Arg Gly	
500 505 510	
agg aac gct acg aag acg gag aat tgg ccc gtg tat gat ctg gag aat	1584
Arg Asn Ala Thr Lys Thr Glu Asn Trp Pro Val Tyr Asp Leu Glu Asn	
515 520 525	
ccc ttg agt atg atc tgg gat gcg aat gtc act tcg tat gcg gcg ccg	1632
Pro Leu Ser Met Ile Trp Asp Ala Asn Val Thr Ser Tyr Ala Ala Pro	
530 535 540	
gat act tgg cgt aag gag ggt att gcg ttg att aat gct aat cgg agg	1680
Asp Thr Trp Arg Lys Glu Gly Ile Ala Leu Ile Asn Ala Asn Arg Arg	
545 550 555 560	
gcg tat cag agg tga	1695
Ala Tyr Gln Arg	

<210> 33
 <211> 564
 <212> PRT
 <213> *Aspergillus niger*

<400> 33

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Ile	Pro	Phe	Ala	Lys	Pro	Pro	Leu	Ala	His	Leu	Arg	Trp	Ala	Asn	Pro
	50					55					60				
Glu	Ser	Leu	Asn	Glu	Ser	Trp	Ser	Gly	Leu	Arg	Pro	Ala	Thr	Gly	Tyr
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Ala	Met	Glu	Cys	Ile	Gly	Tyr	Gly	Ser	Asp	Gln	Lys	Gly	Tyr	Leu	Gln
				85					90					95	
Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Val	Val	Arg	Pro	Ala	Glu	Tyr	Asp
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Asn	Ala	Ser	Leu	Pro	Val	Leu	Val	Trp	Ile	His	Gly	Gly	Gly	Phe	Ala
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Gln	Gly	Gly	Thr	Pro	Asp	Leu	Arg	Tyr	Asn	Leu	Thr	Phe	Ile	Val	Glu
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His	Ser	Val	Asn	Ile	Gly	Gln	Pro	Ile	Ile	Ala	Val	Ser	Val	Ala	Tyr
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Arg	Leu	Gly	Pro	Trp	Gly	Phe	Phe	Asn	Gly	Val	Glu	Leu	Ala	Asn	Glu
				165					170					175	
Gly	Ser	Leu	Asn	Leu	Gly	Leu	Lys	Asp	Gln	Arg	Leu	Ala	Leu	His	Trp
			180					185					190		
Val	Lys	Glu	Asn	Ile	Ala	Gly	Phe	Gly	Gly	Asp	Pro	Ser	Lys	Val	Val
		195					200					205			
Ile	Tyr	Gly	Gln	Ser	Ala	Gly	Ser	Glu	Ser	Val	Gly	Tyr	Gln	Ile	Arg
	210					215					220				
Ala	Tyr	Asn	Gly	Arg	Asp	Asp	Gly	Leu	Phe	Arg	Gly	Gly	Met	Met	Glu
225					230					235					240
Ser	Gly	Ala	Val	Leu	Pro	Gly	Ser	Ala	Leu	Asn	Leu	Thr	Trp	Thr	Tyr
				245					250					255	
Glu	Pro	Trp	Phe	Gln	Gln	Ile	Ala	Asp	Glu	Ala	Gly	Cys	Ser	Gln	Thr
			260					265					270		
Thr	Arg	Lys	Leu	Asp	Cys	Leu	Arg	Arg	Thr	Pro	Phe	Thr	Val	Leu	Asn
		275					280						285		
Asn	Ile	Leu	Asn	Thr	Thr	Ala	Asn	Asp	Thr	Thr	Pro	Tyr	Asn	Trp	Arg
	290					295					300				
Pro	Thr	Val	Asp	Gly	Asp	Phe	Val	Ala	Arg	Tyr	Pro	Ser	Glu	Gln	Leu
305					310					315					320
Asp	Thr	Gly	Asp	Phe	Val	Lys	Val	Pro	Ile	Ile	Ile	Gly	Tyr	Thr	Thr
				325					330					335	
Asp	Glu	Gly	Thr	Thr	Glu	Cys	Pro	Glu	Pro	Val	Asn	Thr	Thr	Ala	Glu
			340					345					350		
Leu	Lys	Glu	Tyr	Leu	Ser	Ser	Thr	Thr	Thr	Tyr	Gly	Trp	Ala	Leu	Asp
		355					360					365			
Ser	Gln	Val	Val	Ser	Ser	Leu	Leu	Asp	Leu	Tyr	Pro	Asn	Thr	Thr	Ser
	370					375					380				
Phe	Gly	Ile	Pro	Ser	Ser	Glu	Glu	Leu	Gly	Gly	Asn	Val	Thr	Phe	Pro
385					390					395					400
Gln	Pro	Tyr	Gly	Ala	Ala	Phe	Arg	Gln	Thr	Ala	Ala	Tyr	Tyr	Gly	Asp
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Ala	Gln	Phe	Ile	Ala	Ala	Thr	Arg	Tyr	Thr	Cys	Glu	Leu	Trp	Ala	Ala
			420					425					430		
His	Asn	Leu	Thr	Ala	Tyr	Cys	Tyr	Arg	Phe	Asn	Thr	Lys	Thr	Asp	Asp

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ataagatata	tggtacatag	tatagatgtg	ttgtgatgtt	attctggcta	ttttgtacac	2340
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<210> 35
 <211> 789
 <212> DNA
 <213> *Aspergillus niger*

<220>
 <221> CDS
 <222> (1)..(789)

<400> 35																
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1 5 10 15																
gcc ctt tcc acc cca ctg gca acc gac gcc gaa aac ctc tac gca cgt	96															
Ala Leu Ser Thr Pro Leu Ala Thr Asp Ala Glu Asn Leu Tyr Ala Arg																
20 25 30																
caa ttc ggc acg ggc tct aca gcc aac gaa ctc gag cag gga agc tgc	144															
Gln Phe Gly Thr Gly Ser Thr Ala Asn Glu Leu Glu Gln Gly Ser Cys																
35 40 45																
aag gat gtg act ctc atc ttt gcg agg ggg tca act gag ctt ggg aat	192															
Lys Asp Val Thr Leu Ile Phe Ala Arg Gly Ser Thr Glu Leu Gly Asn																
50 55 60																
atg ggc acc gta atc ggc ccc cct ctc tgc gac aac ctg aaa tcc aaa	240															
Met Gly Thr Val Ile Gly Pro Pro Leu Cys Asp Asn Leu Lys Ser Lys																
65 70 75 80																
ctc gga tcc gac aaa gtc gcc tgc cag ggt gtc ggc ggc caa tac agc	288															
Leu Gly Ser Asp Lys Val Ala Cys Gln Gly Val Gly Gly Gln Tyr Ser																
85 90 95																
gcc gga ctc gtg cag aat gcc ctg ccc cag aac acc gat ccg ggg agt	336															
Ala Gly Leu Val Gln Asn Ala Leu Pro Gln Asn Thr Asp Pro Gly Ser																
100 105 110																
atc tcc gcc gcg aag cag atg ttc gag gag gcg aat tcg aag tgt ccc	384															
Ile Ser Ala Ala Lys Gln Met Phe Glu Glu Ala Asn Ser Lys Cys Pro																
115 120 125																
aat act aag att gtt gcg ggt ggt tat agt caa gga agc gct gtg att	432															
Asn Thr Lys Ile Val Ala Gly Gly Tyr Ser Gln Gly Ser Ala Val Ile																
130 135 140																
gac aac gcc gtg caa gaa ctc agc acc acc gtg aaa gac caa gtg aag	480															
Asp Asn Ala Val Gln Glu Leu Ser Thr Thr Val Lys Asp Gln Val Lys																
145 150 155 160																
ggg gtc gtg ctc ttc ggg ttc acg aga aac gtg cag gat cac ggg cag	528															
Gly Val Val Leu Phe Gly Phe Thr Arg Asn Val Gln Asp His Gly Gln																
165 170 175																
atc cct aat tac cct aag gat gac gtg aag gtt tat tgt gcc gtg ggc	576															
Ile Pro Asn Tyr Pro Lys Asp Asp Val Lys Val Tyr Cys Ala Val Gly																
180 185 190																
gat ctg gtc tgt gat gat acg ttg gtt gtt acg gcg atg cat ctg acg	624															
Asp Leu Val Cys Asp Asp Thr Leu Val Val Thr Ala Met His Leu Thr																
195 200 205																
tat ggc atg gat gcg ggt gat gcg gcg agc ttt ttg gcc gag aag gtg	672															
Tyr Gly Met Asp Ala Gly Asp Ala Ala Ser Phe Leu Ala Glu Lys Val																
210 215 220																
cag tct tcc agt agt tcg act act agc tcc agc tcg gat gcc gcg agt	720															
Gln Ser Ser Ser Ser Ser Thr Thr Ser Ser Ser Ser Asp Ala Ala Ser																
225 230 235 240																

agt tca tct gct gcg ggg acg tcg tcg tcg ggg ttg tcg gga ctg tct	768
Ser Ser Ser Ala Ala Gly Thr Ser Ser Ser Gly Leu Ser Gly Leu Ser	
245 250 255	
tct ttt ttt gga ggt ctc taa	789
Ser Phe Phe Gly Gly Leu	
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<210> 36
 <211> 262
 <212> PRT
 <213> Aspergillus niger

<400> 36

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Gln Phe Gly Thr Gly Ser Thr Ala Asn Glu Leu Glu Gln Gly Ser Cys	
35 40 45	
Lys Asp Val Thr Leu Ile Phe Ala Arg Gly Ser Thr Glu Leu Gly Asn	
50 55 60	
Met Gly Thr Val Ile Gly Pro Pro Leu Cys Asp Asn Leu Lys Ser Lys	
65 70 75 80	
Leu Gly Ser Asp Lys Val Ala Cys Gln Gly Val Gly Gly Gln Tyr Ser	
85 90 95	
Ala Gly Leu Val Gln Asn Ala Leu Pro Gln Asn Thr Asp Pro Gly Ser	
100 105 110	
Ile Ser Ala Lys Gln Met Phe Glu Glu Ala Asn Ser Lys Cys Pro	
115 120 125	
Asn Thr Lys Ile Val Ala Gly Gly Tyr Ser Gln Gly Ser Ala Val Ile	
130 135 140	
Asp Asn Ala Val Gln Glu Leu Ser Thr Thr Val Lys Asp Gln Val Lys	
145 150 155 160	
Gly Val Val Leu Phe Gly Phe Thr Arg Asn Val Gln Asp His Gly Gln	
165 170 175	
Ile Pro Asn Tyr Pro Lys Asp Asp Val Lys Val Tyr Cys Ala Val Gly	
180 185 190	
Asp Leu Val Cys Asp Asp Thr Leu Val Val Thr Ala Met His Leu Thr	
195 200 205	
Tyr Gly Met Asp Ala Gly Asp Ala Ala Ser Phe Leu Ala Glu Lys Val	
210 215 220	
Gln Ser Ser Ser Ser Ser Thr Thr Ser Ser Ser Asp Ala Ala Ser	
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245 250 255	
Ser Phe Phe Gly Gly Leu	
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<210> 37
 <211> 2981
 <212> DNA
 <213> Aspergillus niger

<400> 37

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cctttcctta taatggctgc cccggcaaac cccaattgc tgtttaggcc agcgagata	180
gcaaattctc cgtctgatta acgatgctaa agctcgctgt tgctcttttt tcgttacttg	240
ccgtgggcaa tgcagcgcca accaaagtgg cccgttccac ggccagtcct acggccaagg	300

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gaatgccgta	tgcccagcag	ccttttaggtg	acttgcgctt	cacggtgcct	cagtccttga	420
acgaaagctg	gagtggcgag	cgcgacgcga	aggaatattc	caatatctgt	gtaggatacg	480
gtgtgagtg	gcaaatcttc	ttcgagagcc	aggccctact	agctgcatcc	tggcactatg	540
aatataatct	aatgggtaga	tctgttagac	cgactcgatt	tggtagccac	agtccgaagc	600
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tatcgccctt	cggcatgggg	cttcttgagt	tccagtcaag	tctggggcac	tggcaatacc	900
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gagtcaggag	ggactattgc	agctagtcca	gccaaactata	ccgggtacca	agcgactat	1140
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gaagttccgt	tcgagaaatt	gaacgctgct	ctcaacacca	ccagtggtaa	ctcggatttc	1260
aatttcgggg	ccgtcattga	tggagatata	atcagggact	ggggcagcct	ccagctagac	1320
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caagaatcaa	gaacccaggg	ggtcaagaga	atctggaagc	gataaagggg	tcttcttttt	2640
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taaccaagtc	cccgattgta	ctacggctac	caaaactaga	atgatgaaaa	tattggagta	2820
cgaaaggaac	taaaccaata	ctaagaaaaa	aaaaaaagag	taaagaaaaa	agagtaaaaa	2880
accaagctcg	gaaagtaaaa	atttccctcg	gtcttgttgt	cattccccta	cctattgaga	2940
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<210> 38

<211> 1686

<212> DNA

<213> *Aspergillus niger*

<220>

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<222> (1)..(1686)

<400> 38

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1					5				10					15		
gca	gcg	cca	acc	aaa	gtg	gcc	cgt	tcc	acg	gcc	agt	cct	acg	gcc	aag	96

Ala	Ala	Pro	Thr	Lys	Val	Ala	Arg	Ser	Thr	Ala	Ser	Pro	Thr	Ala	Lys	
			20					25					30			
gtt	cg	aac	ggt	aca	tat	gtc	gga	gtg	aca	aat	gcg	cat	tac	cag	caa	144
Val	Arg	Asn	Gly	Thr	Tyr	Val	Gly	Val	Thr	Asn	Ala	His	Tyr	Gln	Gln	
		35					40					45				
gat	ttc	ttt	ttg	gga	atg	ccg	tat	gcc	cag	cag	cct	tta	ggt	gac	ttg	192
Asp	Phe	Phe	Leu	Gly	Met	Pro	Tyr	Ala	Gln	Gln	Pro	Leu	Gly	Asp	Leu	
	50					55					60					
cg	ttc	acg	gtg	cct	cag	tcc	ctg	aac	gaa	agc	tgg	agt	ggc	gag	cg	240
Arg	Phe	Thr	Val	Pro	Gln	Ser	Leu	Asn	Glu	Ser	Trp	Ser	Gly	Glu	Arg	
					70					75					80	
gac	gcg	aag	gaa	tat	tcc	aat	atc	tgt	gta	gga	tac	ggt	acc	gac	tcg	288
Asp	Ala	Lys	Glu	Tyr	Ser	Asn	Ile	Cys	Val	Gly	Tyr	Gly	Thr	Asp	Ser	
				85					90					95		
att	tgg	tac	cca	cag	tcc	gaa	gct	tgt	cta	acc	ttg	aat	gtc	atc	cg	336
Ile	Trp	Tyr	Pro	Gln	Ser	Glu	Ala	Cys	Leu	Thr	Leu	Asn	Val	Ile	Arg	
			100					105					110			
gat	tct	tct	gca	aat	gag	aac	tcg	aag	ctc	ccc	gtg	ggc	gtc	tgg	ata	384
Asp	Ser	Ser	Ala	Asn	Glu	Asn	Ser	Lys	Leu	Pro	Val	Gly	Val	Trp	Ile	
			115				120					125				
cat	gga	ggt	ggc	ttc	ttt	gag	gga	tct	agt	gct	gac	cag	cg	tac	aac	432
His	Gly	Gly	Gly	Phe	Phe	Glu	Gly	Ser	Ser	Ala	Asp	Gln	Arg	Tyr	Asn	
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Met	Ser	Ala	Ile	Val	Ala	Asn	Ser	Tyr	Lys	Ile	Gly	Lys	Pro	Phe	Ile	
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gct	gtc	agc	tta	aac	tat	cg	ctt	tcg	gca	tgg	ggc	ttc	ttg	agt	tcc	528
Ala	Val	Ser	Leu	Asn	Tyr	Arg	Leu	Ser	Ala	Trp	Gly	Phe	Leu	Ser	Ser	
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agt	caa	gtc	tgg	ggc	act	ggc	aat	acc	aat	cta	ggt	atc	agg	gat	caa	576
Ser	Gln	Val	Trp	Gly	Thr	Gly	Asn	Thr	Asn	Leu	Gly	Ile	Arg	Asp	Gln	
			180				185						190			
agg	tta	gca	ctc	cat	tgg	atc	aag	gag	aat	atc	gcg	gca	ttc	gga	gga	624
Arg	Leu	Ala	Leu	His	Trp	Ile	Lys	Glu	Asn	Ile	Ala	Ala	Phe	Gly	Gly	
			195				200					205				
gac	cca	gat	aag	atc	act	atc	tgg	ggc	gaa	tct	gcc	gga	gcg	atg	tcc	672
Asp	Pro	Asp	Lys	Ile	Thr	Ile	Trp	Gly	Glu	Ser	Ala	Gly	Ala	Met	Ser	
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gtg	ggt	tat	cac	ctt	gca	gca	tac	ggc	ggt	agg	gac	gat	gga	ctc	ttc	720
Val	Gly	Tyr	His	Leu	Ala	Ala	Tyr	Gly	Gly	Arg	Asp	Asp	Gly	Leu	Phe	
					230					235					240	
cg	gga	gga	att	atg	gag	tca	gga	ggg	act	att	gca	gct	agt	cca	gcc	768
Arg	Gly	Gly	Ile	Met	Glu	Ser	Gly	Gly	Thr	Ile	Ala	Ala	Ser	Pro	Ala	
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Asn	Tyr	Thr	Gly	Tyr	Gln	Ala	His	Tyr	Asp	Glu	Leu	Ala	Gly	Gln	Val	
			260					265					270			
ggt	tgc	tcc	gac	gta	gta	gat	tcg	ttg	cag	tgc	ctg	cg	gaa	gtt	ccg	864
Gly	Cys	Ser	Asp	Val	Val	Asp	Ser	Leu	Gln	Cys	Leu	Arg	Glu	Val	Pro	
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ttc	gag	aaa	ttg	aac	gct	gct	ctc	aac	acc	acc	agt	ggt	aac	tcg	gat	912
Phe	Glu	Lys	Leu	Asn	Ala	Ala	Leu	Asn	Thr	Thr	Ser	Gly	Asn	Ser	Asp	
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ttc	aat	ttc	ggg	ccc	gtc	att	gat	gga	gat	ata	atc	agg	gac	tgg	ggc	960
Phe	Asn	Phe	Gly	Pro	Val	Ile	Asp	Gly	Asp	Ile	Ile	Arg	Asp	Trp	Gly	
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agc	ctc	cag	cta	gac	aag	cat	gaa	ttc	gtc	aaa	gtc	cct	att	ctt	gca	1008
Ser	Leu	Gln	Leu	Asp	Lys	His	Glu	Phe	Val	Lys	Val	Pro	Ile	Leu	Ala	
				325					330					335		
ggt	acc	aat	acc	gac	gaa	ggg	aca	gcc	ttt	ggg	ccc	aca	ggt	atc	aac	1056

Gly	Thr	Asn	Thr	Asp	Glu	Gly	Thr	Ala	Phe	Gly	Pro	Thr	Gly	Ile	Asn	
			340					345					350			
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Thr	Thr	Glu	Glu	Phe	Tyr	Ala	Tyr	Leu	Thr	Asp	Gly	Glu	Ser	Gly	Phe	
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cag	cta	ccc	ccc	acg	atc	gcc	cag	gaa	atc	ctg	cag	ctc	tac	cct	gat	1152
Gln	Leu	Pro	Pro	Thr	Ile	Ala	Gln	Glu	Ile	Leu	Gln	Leu	Tyr	Pro	Asp	
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Asp	Pro	Ala	Leu	Gly	Ile	Pro	Glu	Phe	Leu	Gly	Asp	Thr	Arg	Val	Pro	
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Ser	Lys	Gly	Tyr	Gln	Trp	Arg	Arg	Thr	Cys	Ala	Tyr	Ala	Gly	Asp	Tyr	
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gta	atg	cat	gcc	aac	cgt	cgc	cga	caa	tgt	gag	gcg	tgg	aca	gag	acc	1296
Val	Met	His	Ala	Asn	Arg	Arg	Arg	Gln	Cys	Glu	Ala	Trp	Thr	Glu	Thr	
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tcg	acg	acg	gcg	tac	tgt	tat	cga	ttc	aat	atg	cgt	gcg	gcc	gat	gtc	1344
Ser	Thr	Thr	Ala	Tyr	Cys	Tyr	Arg	Phe	Asn	Met	Arg	Ala	Ala	Asp	Val	
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ccc	atc	ctg	tct	ggc	gcc	acc	cat	ttt	gaa	gaa	ggt	gct	ttt	gta	ttc	1392
Pro	Ile	Leu	Ser	Gly	Ala	Thr	His	Phe	Glu	Glu	Val	Ala	Phe	Val	Phe	
			450			455					460					
aac	aac	att	gca	gga	ctc	ggg	tac	cat	tac	gga	aag	ccg	ttc	gca	ggg	1440
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atg	ccc	gag	tcc	tac	gta	cag	cta	agc	aac	ttg	atg	acc	agc	atg	tgg	1488
Met	Pro	Glu	Ser	Tyr	Val	Gln	Leu	Ser	Asn	Leu	Met	Thr	Ser	Met	Trp	
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gca	tcc	ttc	atc	cac	gat	tta	gac	cct	aat	tcg	ggc	atc	aag	gac	tca	1536
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gct	gta	cag	tgg	caa	ccg	tac	ggg	aag	gat	cag	ccg	ggt	gat	cta	gtg	1584
Ala	Val	Gln	Trp	Gln	Pro	Tyr	Gly	Lys	Asp	Gln	Pro	Val	Asp	Leu	Val	
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Phe	Asp	Ala	Asn	Val	Thr	Ser	Tyr	Ser	Tyr	Met	Glu	Pro	Asp	Thr	Trp	
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cgg	aag	gag	ggg	atc	gac	tat	atc	aat	tcc	gtg	gcc	aac	gcg	tac	tgg	1680
Arg	Lys	Glu	Gly	Ile	Asp	Tyr	Ile	Asn	Ser	Val	Ala	Asn	Ala	Tyr	Trp	
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cga	taa															1686
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<210> 39

<211> 561

<212> PRT

<213> *Aspergillus niger*

<400> 39

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Asp	Phe	Phe	Leu	Gly	Met	Pro	Tyr	Ala	Gln	Gln	Pro	Leu	Gly	Asp	Leu	
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Arg	Phe	Thr	Val	Pro	Gln	Ser	Leu	Asn	Glu	Ser	Trp	Ser	Gly	Glu	Arg	

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Asp	Ala	Lys	Glu	Tyr	Ser	Asn	Ile	Cys	Val	Gly	Tyr	Gly	Thr	Asp
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Ile	Trp	Tyr	Pro	Gln	Ser	Glu	Ala	Cys	Leu	Thr	Leu	Asn	Val	Ile
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Asp	Ser	Ser	Ala	Asn	Glu	Asn	Ser	Lys	Leu	Pro	Val	Gly	Val	Trp
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His	Gly	Gly	Gly	Phe	Phe	Glu	Gly	Ser	Ser	Ala	Asp	Gln	Arg	Tyr
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Met	Ser	Ala	Ile	Val	Ala	Asn	Ser	Tyr	Lys	Ile	Gly	Lys	Pro	Phe
	145				150					155				160
Ala	Val	Ser	Leu	Asn	Tyr	Arg	Leu	Ser	Ala	Trp	Gly	Phe	Leu	Ser
			165						170					175
Ser	Gln	Val	Trp	Gly	Thr	Gly	Asn	Thr	Asn	Leu	Gly	Ile	Arg	Asp
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	195						200					205		Gly
Asp	Pro	Asp	Lys	Ile	Thr	Ile	Trp	Gly	Glu	Ser	Ala	Gly	Ala	Met
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Val	Gly	Tyr	His	Leu	Ala	Ala	Tyr	Gly	Gly	Arg	Asp	Asp	Gly	Leu
	225				230					235				Phe
Arg	Gly	Gly	Ile	Met	Glu	Ser	Gly	Gly	Thr	Ile	Ala	Ala	Ser	Pro
			245						250					255
Asn	Tyr	Thr	Gly	Tyr	Gln	Ala	His	Tyr	Asp	Glu	Leu	Ala	Gly	Gln
			260					265					270	Val
Gly	Cys	Ser	Asp	Val	Val	Asp	Ser	Leu	Gln	Cys	Leu	Arg	Glu	Val
	275					280						285		Pro
Phe	Glu	Lys	Leu	Asn	Ala	Ala	Leu	Asn	Thr	Thr	Ser	Gly	Asn	Ser
	290				295					300				Asp
Phe	Asn	Phe	Gly	Pro	Val	Ile	Asp	Gly	Asp	Ile	Ile	Arg	Asp	Trp
	305				310					315				Gly
Ser	Leu	Gln	Leu	Asp	Lys	His	Glu	Phe	Val	Lys	Val	Pro	Ile	Leu
			325						330					Ala
Gly	Thr	Asn	Thr	Asp	Glu	Gly	Thr	Ala	Phe	Gly	Pro	Thr	Gly	Ile
			340					345					350	Asn
Thr	Thr	Glu	Glu	Phe	Tyr	Ala	Tyr	Leu	Thr	Asp	Gly	Glu	Ser	Gly
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Gln	Leu	Pro	Pro	Thr	Ile	Ala	Gln	Glu	Ile	Leu	Gln	Leu	Tyr	Pro
	370				375						380			Asp
Asp	Pro	Ala	Leu	Gly	Ile	Pro	Glu	Phe	Leu	Gly	Asp	Thr	Arg	Val
	385				390					395				Pro
Ser	Lys	Gly	Tyr	Gln	Trp	Arg	Arg	Thr	Cys	Ala	Tyr	Ala	Gly	Asp
			405						410				415	Tyr
Val	Met	His	Ala	Asn	Arg	Arg	Arg	Gln	Cys	Glu	Ala	Trp	Thr	Glu
			420					425					430	Thr
Ser	Thr	Thr	Ala	Tyr	Cys	Tyr	Arg	Phe	Asn	Met	Arg	Ala	Ala	Asp
	435						440					445		Val
Pro	Ile	Leu	Ser	Gly	Ala	Thr	His	Phe	Glu	Glu	Val	Ala	Phe	Val
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Asn	Asn	Ile	Ala	Gly	Leu	Gly	Tyr	His	Tyr	Gly	Lys	Pro	Phe	Ala
	465				470					475				Gly
Met	Pro	Glu	Ser	Tyr	Val	Gln	Leu	Ser	Asn	Leu	Met	Thr	Ser	Met
			485						490				495	Trp
Ala	Ser	Phe	Ile	His	Asp	Leu	Asp	Pro	Asn	Ser	Gly	Ile	Lys	Asp
			500					505					510	Ser
Ala	Val	Gln	Trp	Gln	Pro	Tyr	Gly	Lys	Asp	Gln	Pro	Val	Asp	Leu
	515						520					525		Val
Phe	Asp	Ala	Asn	Val	Thr	Ser	Tyr	Ser	Tyr	Met	Glu	Pro	Asp	Thr
	530				535					540				Trp
Arg	Lys	Glu	Gly	Ile	Asp	Tyr	Ile	Asn	Ser	Val	Ala	Asn	Ala	Tyr
	545				550					555				Trp
														560

Arg